

GemCore version 5.1.4\_p5\_4578  
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OM protein - protein search, using sw model

Run on: March 17, 2003, 07:13:51 ; Search time 4.06107 seconds  
(without alignments)  
194.050 Million cell updates/sec

Title: US-09-787-082-9  
Perfect score: 119  
Sequence: 1 CCSNPVCHLSNLTNGG 19

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues  
Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SwissProt\_40.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query	Score	Match	Length	ID	Description
1	96	80.7	16	1	CXA2_CONMA	P56636 conus magus
2	61	51.3	66	1	CXA2_CONTE	Q9x2k7 conus texti
3	60.5	50.8	971	1	RECK_MOUSE	Q920j1 mus musculus
4	57.5	48.3	971	1	RECK_HUMAN	Q95980 homo sapien
5	56	47.1	69	1	CXA1_CONTE	Q9x2k6 conus texti
6	49	41.2	588	1	GRN_RAT	P23785 r granulin
7	48.5	40.8	1210	1	EGRF_MOUSE	Q01279 mus musculus
8	48	40.3	16	1	CXA1_CONEP	P56638 conus epic
9	47	39.5	18	1	CXA1_CONER	P50982 conus ermin
10	47	39.5	69	1	OXT1_OXYKI	P83288 oxyopes kit
11	47	39.5	566	1	EST1_PIG	Q29550 sus scrofa
12	45	37.8	16	1	CXA1_CONAL	P56639 conus aulic
13	45	37.8	878	1	PMPI_CHLTR	O84882 chlamydia t
14	45	37.8	2907	1	FBN2_MOUSE	Q61555 mus musculus
15	45	37.8	2911	1	FBN2_HUMAN	P35556 homo sapien
16	44.5	37.4	434	1	SL54_BRAOL	P17841 brassica ol
17	44.5	37.4	686	1	DL4_MOUSE	Q9j171 mus musculus
18	44.5	37.4	2470	1	NTC2_MOUSE	O35516 mus musculus
19	44.5	37.4	2471	1	NTC2_RAT	Q9q30 rattus norv
20	44	37.0	16	1	CXA3_CONAL	P56641 conus aulic
21	44	37.0	16	1	CXAB_CONPE	P50985 conus penna
22	44	37.0	19	1	CXR_CONTU	P58811 conus tulip
23	44	37.0	445	1	AD18_RAT	P97776 rattus norv
24	44	37.0	712	1	FB11_CAEEL	O77469 caenorhabdi
25	44	37.0	719	1	AD18_MOUSE	Q9r157 mus musculus
26	43.5	36.6	986	1	CYGR_ARBP	P11528 arabacia pun
27	43	36.1	452	1	AD11_XENLA	Q9psz3 xenopus lae
28	43	36.1	515	1	APX1_CAEEL	P41990 caenorhabdi
29	43	36.1	525	1	NAB2_YEAST	P32505 saccharomyc
30	43	36.1	586	1	LRE1_YEAST	P25379 saccharomyc
31	43	36.1	719	1	HX1A_MAIZE	P46605 zea mays (m
32	43	36.1	824	1	AD08_HUMAN	P78325 homo sapien
33	42.5	35.7	54	1	IOVO_ANHNO	P05565 anHINGA nov

34	42.5	35.7	54	1	IOVO_CIRAE	P05579 circus aeru
35	42.5	35.7	54	1	IOVO_DRONO	P05560 dromaius no
36	42.5	35.7	54	1	IOVO_GUIGU	P52246 guira guira
37	42.5	35.7	54	1	IOVO_GYPCO	P05578 gyys coprot
38	42.5	35.7	54	1	IOVO_HALAL	P52268 haliaetetus
39	42.5	35.7	54	1	IOVO_HALIN	P05577 haliastur i
40	42.5	35.7	54	1	IOVO_PAVMU	P52263 pavo muticu
41	42.5	35.7	54	1	IOVO_PASU	P05564 phalacrocor
42	42.5	35.7	54	1	IOVO_PXCAD	P52257 pygoscelis
43	42.5	35.7	54	1	IOVO_RHEAM	P05558 rhea americ
44	42.5	35.7	54	1	IOVO_SPHHU	P05563 spheniscus
45	42.5	35.7	56	1	IOVO_PAVCR	P05609 pavo crista

ALIGNMENTS

RESULT 1  
CXA2\_CONMA  
ID CXA2\_CONMA STANDARD; PRT; 16 AA.  
AC P56636;  
DT 15-DEC-1998 (Rel. 37, Created)  
DT 15-DEC-1998 (Rel. 37, Last sequence update)  
DT 15-JUN-2002 (Rel. 41, Last annotation update)  
DE Alpha-conotoxin MII (M2).  
OS Conus magus (Magus cone).  
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Caenogastropoda;  
OC Neogastropoda; Conoidea; Conidae; Conus.  
OX NCBI\_Taxid=6492;  
RN [1]  
RP SEQUENCE, AND SYNTHESIS.  
RC TISSUE=Venom;  
RX MEDLINE=96205934; PubMed=8631783;  
RA Cartier G.E., Yoshikami D., Gray W.R., Luo S., Olivera B.M.,  
RA McIntosh J.M.;  
RT "A new alpha-conotoxin which targets alpha3beta2 nicotinic  
RT acetylcholine receptors.";  
RL J. Biol. Chem. 271:7522-7528(1996).  
RN [2]  
RP STRUCTURE BY NMR.  
RX MEDLINE=98062282; PubMed=9398298;  
RA Shon K.-J., Koerber S.C., Rivier J.E., Olivera B.M., McIntosh J.M.;  
RT "Three-dimensional solution structure of alpha-conotoxin MII, an  
RT alpha3beta2 neuronal nicotinic acetylcholine receptor-targeted  
RT ligand.";  
RL Biochemistry 36:15693-15700(1997).  
RN [3]  
RP STRUCTURE BY NMR.  
RX MEDLINE=99060038; PubMed=9843366;  
RA Hill J.M., Oomen C.J., Miranda L.P., Bingham J.-P., Alewood P.F.,  
RA Craik D.J.;  
RT "Three-dimensional solution structure of alpha-conotoxin MII by NMR  
RT spectroscopy: effects of solution environment on helicity.";  
RL Biochemistry 37:15621-15630(1998).  
CC -!- FUNCTION: ALPHA-CONOTOXINS ACT ON POSTSYNAPTIC MEMBRANES, THEY  
CC BIND TO THE NICOTINIC ACETYLCHOLINE RECEPTORS (NACHR) AND THUS  
CC INHIBIT THEM. THIS PEPTIDE BLOCKS MAMMALIAN NICOTINIC  
CC ACETYLCHOLINE RECEPTORS COMPOSED OF ALPHA-3/BETA-2 SUBUNITS. IT  
CC HAS AN ACTIVITY 2 TO 4 ORDERS OF MAGNITUDE LESS POTENT ON OTHER  
CC NACHR SUBUNIT COMBINATIONS.  
CC -!- SUBCELLULAR LOCATION: Secreted.  
CC -!- TISSUE SPECIFICITY: Expressed by the venom duct.  
CC -!- SIMILARITY: BELONGS TO THE A-SUPERFAMILY OF CONOTOXINS. ALPHA-TYPE  
CC FAMILY.  
DR PDB; IMII; 21-OCT-98.  
DR PDB; IM2C; 13-JAN-99.  
KW Postsynaptic neurotoxin; Neurotoxin; Toxin;  
KW Acetylcholine receptor inhibitor; Amidation; 3D-structure.  
FT DISULFID 2 8  
FT DISULFID 3 16  
FT MOD\_RES 16 16  
FT SEQUENCE 16 AA; 1716 MW; 282AEF190166CAF9 CRC64;

Query Match 80.7%; Score 96; DB 1; Length 16;  
Best Local Similarity 100.0%; Pred. No. 1.8e-07;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCNPNVCHLEHSLC 15  
|||||  
Db 2 CCNPNVCHLEHSLC 16

## RESULT 2

CXAX2\_CONTE STANDARD; PRT; 66 AA.  
ID Q9XZK7:  
AC 16-OCT-2001 (Rel. 40, Created)  
DT 16-OCT-2001 (Rel. 40, Last sequence update)  
DT 15-JUN-2002 (Rel. 41, Last annotation update)  
DE Alpha-type conotoxin Tx2 precursor.  
OS Conus textile (Cloth-of-gold cone).  
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Caenogastropoda;  
OC Neogastropoda; Conoidea; Conidae; Conus.  
OX NCBI\_TaxID=6494;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE-Venom duct;  
RX MEDLINE=20037955; PubMed=10573284;  
RA Lu B.-S., Yu F., Zhao D., Huang P.-T., Huang C.-F.;  
RT "Conopeptides from Conus striatus and Conus textile by cDNA  
cloning";  
RL Peptides 20:1139-1144(1999).  
CC -!- FUNCTION: Alpha-conotoxins act on postsynaptic membranes, they  
bind to the nicotinic acetylcholine receptors (nAChR) and thus  
inhibit them (By similarity).  
CC -!- SUBCELLULAR LOCATION: Secreted.  
CC -!- TISSUE SPECIFICITY: Expressed by the venom duct.  
CC -!- SIMILARITY: BELONGS TO THE A-SUPERFAMILY OF CONOTOXINS. ALPHA-TYPE  
FAMILY.

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EMBL; AF146353; RAD31913.1; -;  
DR Postsynaptic neurotoxin; Neurotoxin; Toxin;  
KW Acetylcholine receptor inhibitor; Signal.  
FT SIGNAL 1 21  
FT PROPEP 22 48  
FT PEPTIDE 49 66 ALPHA-TYPE CONOTOXIN TX2.  
FT DISULFID 51 57 BY SIMILARITY.  
FT DISULFID 52 65 BY SIMILARITY.  
SQ SEQUENCE 66 AA; 7254 MW; EDDBS9BBAB94F26F CRC64;

Query Match 51.3%; Score 61; DB 1; Length 66;  
Best Local Similarity 46.7%; Pred. No. 0.039;  
Matches 7; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

QY 1 CCNPNVCHLEHSLC 15  
|||||  
Db 51 CCNPNVCHLEHSLC 65

## RESULT 3

RECK\_MOUSE STANDARD; PRT; 971 AA.  
ID Q9Z0J1:  
AC 15-JUN-2002 (Rel. 41, Created)  
DT 15-JUN-2002 (Rel. 41, Last sequence update)  
DT 15-JUN-2002 (Rel. 41, Last annotation update)  
DE Reversion-inducing cysteine-rich protein with kazal motifs precursor  
(mRECK).

GN RECK.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=99007295; PubMed=9789069;  
RA Takahashi C., Sheng Z., Horan T.P., Kitayama H., Makl M., Hitomi K.,  
RA Kitaura Y., Takai S., Sasahara R.M., Horimoto A., Ikawa Y.,  
RA Ratzkin B.J., Arikawa T., Noda M.;  
RT "Regulation of matrix metalloproteinase-9 and inhibition of tumor  
invasion by the membrane-anchored glycoprotein RECK";  
RL Proc. Natl. Acad. Sci. U.S.A. 95:13221-13226(1998).  
CC -!- FUNCTION: Negatively regulates matrix metalloproteinase-9 (MMP-9)  
by suppressing MMP-9 secretion, and by direct inhibition of its  
enzymatic activity. RECK down-regulation by oncogenic signals may  
facilitate tumor invasion and metastasis. Appears to also  
regulate MMP-2 and MT1-MMP, which are involved in cancer  
progression (By similarity).  
CC -!- SUBUNIT: Interacts with MMP-9.  
CC -!- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor.  
CC -!- DEVELOPMENTAL STAGE: In E10.5 embryos the RECK protein is widely  
expressed in mesenchymal tissues and is relatively abundant in the  
marginal zone of the neural tube and large blood vessels such as  
the aorta.  
CC -!- SIMILARITY: CONTAINS 3 KAZAL-LIKE DOMAINS.  
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EMBL; AB006960; BAA34061.1; -;  
DR MGD; MGI:1855698; Reck.  
DR InterPro; IPR002350; kazal.  
DR Pfam; PF00050; kazal; 2.  
DR SMART; SM00280; KAZAL; 2.  
DR PROSITE; PS00282; KAZAL; 1.  
KW Signal; Glycoprotein; GPI-anchor; Serine protease inhibitor;  
KW Membrane; Anti-oncogene; Repeat.  
FT SIGNAL 1 22  
FT CHAIN 23 942  
FT PROPEP 943 971  
FT LIPID 942 942  
FT DOMAIN 633 677 KAZAL-LIKE 1.  
FT DOMAIN 704 750 KAZAL-LIKE 2 (DEGENERATE).  
FT DOMAIN 751 787 KAZAL-LIKE 3 (DEGENERATE).  
FT DOMAIN 37 338 5 X KNOT REPEATS.  
FT REPEAT 37 84 KNOT 1.  
FT REPEAT 104 141 KNOT 2.  
FT REPEAT 151 197 KNOT 3.  
FT REPEAT 216 263 KNOT 4.  
FT REPEAT 292 338 KNOT 5.  
FT DISULFID 635 654 BY SIMILARITY.  
FT DISULFID 633 658 BY SIMILARITY.  
FT DISULFID 643 677 BY SIMILARITY.  
FT CARBOHYD 39 39 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 86 86 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 200 200 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 297 297 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 352 352 N-LINKED (GLCNAC. . .) (POTENTIAL).  
SQ SEQUENCE 971 AA; 106134 MW; 2FC8EBE38A20F86D CRC64;

Query Match 50.8%; Score 60.5; DB 1; Length 971;  
Best Local Similarity 68.8%; Pred. No. 0.45;  
Matches 11; Conservative 2; Mismatches 0; Indels 3; Gaps 1;

QY 4 NPVC---HLEHSLC 16

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Db 721 DPVCDTHMEHSLNCT 736
      :||| :|||
RESULT 4
RECK_HUMAN STANDARD; PRT; 971 AA.
AC O95980; Q8WX37;
DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DE Reversion-inducing cysteine-rich protein with kazal motifs precursor
DE (hRECK) (Suppressor of tumorigenicity 15) (ST15).
GN RECK.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
[1]
SEQUENCE FROM N.A., AND N-GLYCOSYLATION.
RP TISSUE=Fibroblast;
RX MEDLINE=99007295; PubMed=9789069;
RA Takahashi C., Sheng Z., Horan T.P., Kitayama H., Maki M., Hitomi K.,
RA Kitaura Y., Takai S., Sasahara R.M., Horimoto A., Ikawa Y.,
RA Ratzkin B.J., Arakawa T., Noda M.;
RT "Regulation of matrix metalloproteinase-9 and inhibition of tumor
RT invasion by the membrane-anchored glycoprotein RECK.";
RL Proc. Natl. Acad. Sci. U.S.A. 95:13221-13226(1998).
[2]
SEQUENCE OF 363-971 FROM N.A.
RP Kimberley A.;
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: Negatively regulates matrix metalloproteinase-9 (MMP-9)
CC by suppressing MMP-9 secretion and by direct inhibition of its
CC enzymatic activity. RECK down-regulation by oncogenic signals may
CC facilitate tumor invasion and metastasis. Appears to also
CC regulate MMP-2 and MT1-MMP, which are involved in cancer
CC progression.
CC -1- SUBUNIT: Interacts with MMP-9.
CC -1- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor.
CC -1- TISSUE SPECIFICITY: Expressed in various tissues and untransformed
CC cells. It is undetectable in tumor-derived cell lines and
CC oncogenically transformed cells.
CC -1- SIMILARITY: CONTAINS 3 KAZAL-LIKE DOMAINS.
CC
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CC
CC EMBL: D50406; BAA34060.1; -.
CC EMBL: AL158830; CAD13384.1; -.
CC Genbank: HGNC:11345; RECK.
CC MIM: 605227; -.
CC HSP: P80424; IAN1.
CC InterPro: IPR002350; kazal.
CC SMART: SM00280; KAZAL; 3.
CC SMART: SM00011; VWC_def; 1.
CC PROSITE: PS00282; KAZAL; 1.
KW Signal; Glycoprotein; GPI-anchor; Serine protease inhibitor;
KW Membrane; Anti-oncogene; Repeat.
FT SIGNAL 1 22 POTENTIAL.
FT CHAIN 23 942 REVERSION-INDUCING CYSTEINE-RICH PROTEIN
FT WITH KAZAL MOTIFS.
FT PROPEP 943 971 REMOVED IN MATURE FORM (POTENTIAL).
FT LIPID 942 942 GPI-ANCHOR (POTENTIAL).
FT DOMAIN 632 677 KAZAL-LIKE 1.
FT DOMAIN 708 750 KAZAL-LIKE 2 (DEGENERATE).
FT DOMAIN 753 787 KAZAL-LIKE 3 (DEGENERATE).
FT DOMAIN 37 338 5 X KNOT REPEATS.

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Query Match 48.3%; Score 57.5; DB 1; Length 971;
Best Local Similarity 62.5%; Pred. No. 1.2;
Matches 10; Conservative 3; Mismatches 0; Indels 3; Gaps 1;

QY 4 NPVC---HLEHSLNCT 16
      :||| :|||
Db 721 DPVCDTHMEHSLNCT 736
      :||| :|||
RESULT 5
CXAL_CONTE STANDARD; PRT; 59 AA.
ID QXZK6;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Alpha-type conotoxin Tx1 precursor.
OS Conus textile (Cloth-of-gold cone).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Caenogastropoda;
OC Neogastropoda; Conoidea; Conidae; Conus.
OX NCBI_TaxID=6494;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Venom duct.
RX MEDLINE=20037955; PubMed=10573284;
RA Lu B.-S., Yu F., Zhao D., Huang P.-T., Huang C.-F.;
RT "Conopeptides from Conus striatus and Conus textile by cDNA
RT cloning.";
RL Peptides 20:1139-1144(1999).
CC -1- FUNCTION: Alpha-conotoxins act on postsynaptic membranes, they
CC bind to the nicotinic acetylcholine receptors (nAChR) and thus
CC inhibit them (by similarity).
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- TISSUE SPECIFICITY: Expressed by the venom duct.
CC -1- SIMILARITY: BELONGS TO THE A-SUPERFAMILY OF CONOTOXINS. ALPHA-TYPE
CC FAMILY.
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CC
CC EMBL: AF146352; AAD31912.1; -.
CC Postsynaptic neurotoxin; Neurotoxin; Toxin;
KW Acetylcholine receptor inhibitor; Signal; Amidation.
FT SIGNAL 1 21 POTENTIAL.
FT PROPEP 22 48 POTENTIAL.
FT PROPEP 49 66 ALPHA-TYPE CONOTOXIN TX1.
FT DISULFID 51 57 BY SIMILARITY.
FT DISULFID 52 65 BY SIMILARITY.
FT MOD_RES 66 66 AMIDATION (G-67 PROVIDE AMIDE GROUP).
FT SEQUENCE 69 AA; 7442 MW; E36CE90BF1B56B0 CRC64;
Query Match 47.1%; Score 56; DB 1; Length 69;
Best Local Similarity 52.6%; Pred. No. 0.2;

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Matches 10; Conservative 2; Mismatches 5; Indels 2; Gaps 1;

QY 1 CCSPVCHLEHSLNCTNGG 19  
 ||||| | : | | | |  
 Db 51 CCSDPRCNSHPCLC--GG 67

RESULT 6  
 GRN\_RAT GRN\_RAT STANDARD; PRT; 588 AA.  
 AC P23785;  
 DT 01-NOV-1991 (Rel. 20, Created)  
 DT 01-DEC-1992 (Rel. 24, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Granulins precursor (Acrogranin) [Contains: Granulin 1 (Granulin G);  
 DE Granulin 2 (Granulin F); Granulin 3 (Granulin B) (Epithelin 2);  
 DE Granulin 4 (Granulin A) (Epithelin 1); Granulin 5 (Granulin C);  
 DE Granulin 6 (Granulin D); Granulin 7 (Granulin E)].  
 GN GRN.  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 OX NCBI\_TaxID=10116;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Kidney;  
 RX MEDLINE=94062640; PubMed=8243292;  
 RA Bhandari V., Giald A., Bateman A.;  
 RT "The complementary deoxyribonucleic acid sequence, tissue  
 RT distribution, and cellular localization of the rat granulin  
 RT precursor.";  
 RL Endocrinology 133:2682-2689(1993).  
 RN [2]  
 RP SEQUENCE FROM N.A., AND SEQUENCE OF 204-259 AND 278-334.  
 RC TISSUE=Kidney;  
 RX MEDLINE=92317004; PubMed=1618805;  
 RA Plozman G.D., Green J.M., Neubauer M.G., Buckley S.D., McDonald V.L.,  
 RA Todaro G.J., Shoyab M.;  
 RT "The epithelin precursor encodes two proteins with opposing  
 RT activities on epithelial cell growth.";  
 RL J. Biol. Chem. 267:13073-13078(1992).  
 RN [3]  
 RP SEQUENCE OF 204-225 AND 279-299.  
 RX MEDLINE=91045907; PubMed=2236009;  
 RA Shoyab M., McDonald V.L., Byles C., Todaro G.J., Plozman G.D.;  
 RA "Epithelins 1 and 2: isolation and characterization of two  
 RT cysteine-rich growth-modulating proteins.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 87:7912-7916(1990).  
 RN [4]  
 RP SEQUENCE OF 278-328.  
 RC TISSUE=Bone marrow;  
 RX MEDLINE=91097544; PubMed=2268320;  
 RA Bateman A., Belcourt D.R., Bennett H.P., Lazure C., Solomon S.;  
 RA "Granulins, a novel class of peptide from leukocytes.";  
 RL Biochem. Biophys. Res. Commun. 173:1161-1168(1990).  
 CC -1- FUNCTION: GRANULINS HAVE POSSIBLE CYTOKINE-LIKE ACTIVITY. THEY MAY  
 CC PLAY A ROLE IN INFLAMMATION, WOUND REPAIR, AND TISSUE REMODELING.  
 CC -1- TISSUE SPECIFICITY: UBICUITOUS; MOST ABUNDANT IN THE SPLEEN AND  
 CC SEVERAL TISSUES OF ENDOCRINE SIGNIFICANCE.  
 CC -1- PTM: GRANULINS ARE DISULFIDE BRIDGED.  
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 CC  
 CC EMBL; M97750; AAA16903.1; -  
 CC DR EMBL; X62322; CAA44198.1; -  
 CC DR EMBL; A36199; A36199.  
 CC DR PIR; B36199; B36199.

DR PIR; E36698; E36698.  
 DR InterPro; IPR000118; Granulin.  
 DR Pfam; PF00396; granulin; 7.  
 DR SMART; SM00277; GRAN; 7.  
 DR PROSITE; PS00799; GRANULINS; 7. Signal.  
 KW Cytokine; Repeat; Glycoprotein; Signal.  
 FT SIGNAL 1 17  
 FT CHAIN 18 588  
 FT PEPTIDE 58 113  
 FT PEPTIDE 122 178  
 FT PEPTIDE 204 259  
 FT PEPTIDE 278 334  
 FT PEPTIDE 361 413  
 FT PEPTIDE 413 492  
 FT PEPTIDE 512 567  
 FT CARBOHYD 38 38  
 FT CARBOHYD 372 372  
 FT CARBOHYD 525 525  
 FT CONFLICT 201 201  
 FT CONFLICT 307 308  
 FT CONFLICT 324 324  
 FT CONFLICT 388 388  
 SQ SEQUENCE 588 AA; 63369 MW; 113D434F7E099B31 CRC64;

Query Match 41.2%; Score 49; DB 1; Length 588;  
 Best Local Similarity 45.0%; Pred. No. 11;  
 Matches 9; Conservative 2; Mismatches 7; Indels 2; Gaps 1;

QY 1 CCSPVCHLEHSLNCTNG 18  
 || | | | | | | | |  
 Db 385 CCSPPEAVVCLDHCPCQG 404

RESULT 7  
 EGFR\_MOUSE  
 ID EGFR\_MOUSE STANDARD; PRT; 1210 AA.  
 AC Q01279;  
 DT 01-FEB-1996 (Rel. 33, Created)  
 DT 01-FEB-1996 (Rel. 33, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Epidermal growth factor receptor precursor (EC 2.7.1.112).  
 GN EGFR.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=BALB/c; TISSUE=Liver;  
 RX MEDLINE=93026370; PubMed=1408137;  
 RA Avivi A., Skorecki K., Yayon A., Givol D.;  
 RT "Promoter region of the murine fibroblast growth factor receptor 2  
 RT (bek/KGFR) gene.";  
 RL Oncogene 7:1957-1962(1992).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=BALB/c, and CD-1; TISSUE=Liver, and Decidua;  
 RX MEDLINE=93126380; PubMed=7678348;  
 RA Parla B.C., Das S.K., Andrews G.K., Dey S.K.;  
 RT "Expression of the epidermal growth factor receptor gene is regulated  
 RT in mouse blastocysts during delayed implantation.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 90:55-59(1993).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=BALB/c; TISSUE=Liver;  
 RA Hibbs M.L.;  
 RL Submitted (APR-1994) to the EMBL/GenBank/DBJ databases.  
 RN [4]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=B6/C3; TISSUE=Liver;  
 RX MEDLINE=94170986; PubMed=8125255;  
 RA Luetke N.C., Phillips H.K., Qiu T.H., Copeland N.G., Earp H.S.,  
 RA Jenkins N.A., Lee D.C.;

RT "The mouse waved-2 phenotype results from a point mutation in the EGF  
 RT receptor tyrosine kinase.";  
 RL Genes Dev. 8:399-413(1994).  
 RN [5]  
 RP SEQUENCE OF 1-714 FROM N.A.  
 RC TISSUE-Brain;  
 RX MEDLINE-91232866; PubMed-2030916;  
 RA Avivi A., Lax I., Ullrich A., Schlessinger J., Givol D., Morse B.;  
 RT "Comparison of EGF receptor sequences as a guide to study the ligand  
 RT binding site.";  
 RL Oncogene 6:673-676(1991).  
 RN [6]  
 RP SEQUENCE OF 969-1117 FROM N.A.  
 RC STRAIN=C3H;  
 RA Bisinger D.P., Serrero G.;  
 RL Submitted (JUN-1992) to the EMBL/GenBank/DBJ databases.  
 CC -!- FUNCTION: THE EGF RECEPTOR MEDIATES THE BIOLOGICAL SIGNAL OF EGF,  
 CC AND ALSO OF TGF-ALPHA, AMPHIREGULIN, HEPARIN-BINDING EGF, GP30 AND  
 CC VACCINIA VIRUS GROWTH FACTOR (BY SIMILARITY).  
 CC -!- CATALYTIC ACTIVITY: ATP + a protein tyrosine - ADP + protein  
 CC tyrosine phosphate.  
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein.  
 CC -!- MISCELLANEOUS: Binding of EGF to the receptor leads to  
 CC dimerization, internalization of the EGF-receptor complex,  
 CC induction of the tyrosine kinase activity, stimulation of cell DNA  
 CC synthesis, and cell proliferation.  
 CC -!- SIMILARITY: BELONGS TO THE EGF RECEPTOR FAMILY.  
 CC -----  
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 CC -----  
 CC EMBL; X78987; CAA55587.1; -;  
 CC EMBL; U03425; AAA17899.1; -;  
 CC EMBL; X59698; CAA42219.1; -;  
 CC EMBL; L06864; AAA53029.1; -;  
 CC EMBL; Z12608; CAA78249.1; -;  
 CC HSSP; P11362; IFGK.  
 CC MGD; MGI:95294; Egfr.  
 CC InterPro: IPR000494; EGFR\_L\_domain.  
 CC InterPro: IPR000719; Euk\_pkinase.  
 CC InterPro: IPR002174; Furin-like.  
 CC InterPro: IPR001245; Tyr\_pkinase.  
 CC Pfam; PF00069; pkinase; 1.  
 CC Pfam; PF00757; Furin-like; 1.  
 CC Pfam; PF01030; Recep\_L\_domain; 2.  
 CC ProDom; PD000001; Euk\_pkinase; 1.  
 CC SMART; SM00261; FU; 3.  
 CC SMART; SM00219; TyrKc; 1.  
 CC PROSITE; PS00107; PROTEIN\_KINASE\_ATP; 1.  
 CC PROSITE; PS00109; PROTEIN\_KINASE\_TYR; 1.  
 CC PROSITE; PS50011; PROTEIN\_KINASE\_DOM; 1.  
 CC Transmembrane; Glycoprotein; Receptor; Signal; Transferase;  
 KW Tyrosine-protein kinase; ATP-binding; Phosphorylation; Repeat.  
 FT SIGNAL 1 24 POTENTIAL.  
 FT CHAIN 25 1210 EPIDERMAL GROWTH FACTOR RECEPTOR.  
 FT DOMAIN 25 647 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 648 670 POTENTIAL.  
 FT DOMAIN 671 1210 CYTOPLASMIC (POTENTIAL).  
 FT REPEAT 75 300 APPROXIMATE.  
 FT REPEAT 390 600 APPROXIMATE.  
 FT DOMAIN 1028 1071 SER-RICH.  
 FT DOMAIN 714 981 PROTEIN KINASE.  
 FT NP\_BIND 720 728 ATP (BY SIMILARITY).  
 FT BINDING 747 747 ATP (BY SIMILARITY).  
 FT ACT\_SITE 839 839 BY SIMILARITY.  
 FT DISULFID 190 199 BY SIMILARITY.  
 FT DISULFID 194 207 BY SIMILARITY.  
 FT DISULFID 215 223 BY SIMILARITY.

FT DISULFID 219 231 BY SIMILARITY.  
 FT DISULFID 232 240 BY SIMILARITY.  
 FT DISULFID 236 248 BY SIMILARITY.  
 FT DISULFID 251 260 BY SIMILARITY.  
 FT DISULFID 264 291 BY SIMILARITY.  
 FT DISULFID 295 307 BY SIMILARITY.  
 FT DISULFID 311 326 BY SIMILARITY.  
 FT DISULFID 329 333 BY SIMILARITY.  
 FT DISULFID 506 515 BY SIMILARITY.  
 FT DISULFID 510 523 BY SIMILARITY.  
 FT DISULFID 526 535 BY SIMILARITY.  
 FT DISULFID 539 555 BY SIMILARITY.  
 FT DISULFID 558 571 BY SIMILARITY.  
 FT DISULFID 562 579 BY SIMILARITY.  
 FT DISULFID 582 591 BY SIMILARITY.  
 FT DISULFID 595 617 BY SIMILARITY.  
 FT DISULFID 620 628 BY SIMILARITY.  
 FT DISULFID 624 636 BY SIMILARITY.  
 FT MOD\_RES 680 680 PHOSPHORYLATION (BY PKC) (BY SIMILARITY).  
 FT MOD\_RES 1092 1092 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).  
 FT MOD\_RES 1110 1110 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).  
 FT MOD\_RES 1172 1172 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).  
 FT MOD\_RES 1197 1197 PHOSPHORYLATION (AUTO-, MAJOR SITE) (BY SIMILARITY).  
 FT CARBOHYD 128 128 N-LINKED (GLCNAC. .) (POTENTIAL).  
 FT CARBOHYD 175 175 N-LINKED (GLCNAC. .) (POTENTIAL).  
 FT CARBOHYD 196 196 N-LINKED (GLCNAC. .) (POTENTIAL).  
 FT CARBOHYD 352 352 N-LINKED (GLCNAC. .) (POTENTIAL).  
 FT CARBOHYD 413 413 N-LINKED (GLCNAC. .) (POTENTIAL).  
 FT CARBOHYD 444 444 N-LINKED (GLCNAC. .) (POTENTIAL).  
 FT CARBOHYD 528 528 N-LINKED (GLCNAC. .) (POTENTIAL).  
 FT CARBOHYD 568 568 N-LINKED (GLCNAC. .) (POTENTIAL).  
 FT CARBOHYD 603 603 N-LINKED (GLCNAC. .) (POTENTIAL).  
 FT CARBOHYD 623 623 N-LINKED (GLCNAC. .) (POTENTIAL).  
 FT CONFLICT 19 19 C -> S (IN REF. 2).  
 FT CONFLICT 539 539 C -> W (IN REF. 5).  
 FT CONFLICT 991 991 L -> F (IN REF. 4).  
 FT CONFLICT 1116 1117 HP -> DR (IN REF. 6).  
 SQ SEQUENCE 1210 AA; 134853 MW; 690E20D46DF2D2F5 CRC64;  
 Query Match 40.8%; Score 48.5; DB 1; Length 1210;  
 Best Local Similarity 62.5%; Pred. No. 24;  
 Matches 10; Conservative 2; Mismatches 3; Indels 1; Gaps 1;  
 QY 3 SNPYCHLEHSNLTNG 18  
 : | | | | | : | | | | |  
 Db 613 ANNVCHECHAN-CTYG 627  
 RESULT 8  
 CXAL\_CONEP STANDARD; PRT; 16 AA.  
 ID CXAL\_CONEP  
 AC P56638;  
 DT 15-DEC-1998 (Rel. 37, Created)  
 DT 15-DEC-1998 (Rel. 37, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Alpha-conotoxin EpiI.  
 OS Conus episcopatus (Bishop's cone).  
 OC Eukaryota; Metazoa; Mollusca; Gastropoda; Caenogastropoda;  
 OC Neogastropoda; Conoidea; Conidae; Conus.  
 OX NCBI\_TaxID=88764;  
 RN [1]  
 RP X-RAY CRYSTALLOGRAPHY (1.1 ANGSTROMS).  
 RX MEDLINE-98376423; PubMed-9708977;  
 RA Hu S.H., Loughnan M., Miller R., Weeks C.M., Blessing R.H.,  
 RA Alewood P.F., Lewis R.J., Martin J.L.;  
 RT "The 1.1-A resolution crystal structure of [Tyr15]EpiI, a novel  
 RL alpha-conotoxin from Conus episcopatus, solved by direct methods.";  
 RL Biochemistry 37:11425-11433(1998).  
 CC -!- FUNCTION: ALPHA-CONOTOXINS ACT ON POSTSYNAPTIC MEMBRANES, THEY  
 CC BIND TO THE NICOTINIC ACETYLCHOLINE RECEPTORS (NACHR) AND THUS  
 CC INHIBIT THEM. THIS PEPTIDE BLOCKS MAMMALIAN NICOTINIC  
 CC ACETYLCHOLINE RECEPTORS COMPOSED OF ALPHA-3/BETA-2 AND ALPHA-



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DR EMBL; X63323; CAA44929.1; -.  
DR HSSP; P21836; 1MAH.  
DR InterPro; IPR002018; Carboxylesterase.  
DR InterPro; IPR00379; Ser\_eسترs\_site.  
DR Pfam; PF00135; Coesterase; 1.  
DR PROSITE; PS00122; CARBOXYLESTERASE\_B.1; 1.  
DR PROSITE; PS00941; CARBOXYLESTERASE\_B.2; 1.  
KW Glycoprotein; Hydrolase; Serine esterase; Endoplasmic reticulum;  
KW Signal; Multigene family.  
FT SIGNAL 1 18 BY SIMILARITY.  
FT CHAIN 19 566 LIVER CARBOXYLESTERASE.  
FT ACT\_SITE 222 566 CHARGE RELAY SYSTEM (BY SIMILARITY).  
FT ACT\_SITE 467 566 CHARGE RELAY SYSTEM (BY SIMILARITY).  
FT DISULFID 88 117 BY SIMILARITY.  
FT DISULFID 274 285 BY SIMILARITY.  
FT SITE 563 566 PREVENT SECRETION FROM ER (POTENTIAL).  
FT CARBOHYD 80 80 N-LINKED (GLCNAC...) (POTENTIAL).  
SQ SEQUENCE 566 AA; 62016 MW; BE046545307DEDE5 CRC64;

Query Match 39.5%; Score 47; DB 1; Length 566;  
Best Local Similarity 50.0%; Pred. No. 21;  
Matches 9; Conservative 2; Mismatches 7; Indels 0; Gaps 0;

QY 1 CCSPNVPCHLEHSLCTNG 18  
|| :|| :|| :|| :||  
DB 88 CCQDPVVEQMTSLFTNG 105

## RESULT 12

ID CXAL\_CONAL STANDARD; PRT; 16 AA.  
AC P56639;  
DT 15-DEC-1998 (Rel. 37, Created)  
DT 15-DEC-1998 (Rel. 37, Last sequence update)  
DT 15-JUN-2002 (Rel. 41, Last annotation update)  
DE Alpha-conotoxin AuiA.  
OS Conus aulicus (Court cone).  
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Caenogastropoda;  
OC Neogastropoda; Conoidea; Conidae; Conus.  
OX NCBI\_TaxID=89437;  
RN [1]  
RP SEQUENCE, SYNTHESIS, AND MASS SPECTROMETRY.  
RC TISSUE=Venom;  
RX MEDLINE=99003392; PubMed=9786965;  
RA Luo S., Kulak J.M., Cartier G.E., Jacobsen R.B., Yoshikami D.,  
RA Olivera B.M., McIntosh J.M.;  
RT "Alpha-conotoxin AuiB selectively blocks alpha3 beta4 nicotinic  
RT acetylcholine receptors and nicotine-evoked norepinephrine release.";  
RL J. Neurosci. 18:8571-8579(1998).  
CC -!- FUNCTION: ALPHA-CONOTOXINS ACT ON POSTSYNAPTIC MEMBRANES, THEY  
CC BIND TO THE NICOTINIC ACETYLCHOLINE RECEPTORS (NACHR) AND THUS  
CC INHIBIT THEM. THIS PEPTIDE BLOCKS MAMMALIAN NICOTINIC  
CC ACETYLCHOLINE RECEPTORS COMPOSED OF ALPHA-3/BETA-4 SUBUNITS.  
CC -!- SUBCELLULAR LOCATION: Secreted.  
CC -!- TISSUE SPECIFICITY: Expressed by the venom duct.  
CC -!- MASS SPECTROMETRY: MW=1725.6; METHOD=Electrospray.  
CC -!- SIMILARITY: BELONGS TO THE A-SUPERFAMILY OF CONOTOXINS. ALPHA-TYPE  
CC FAMILY.  
DR HSSP; P50984; 1PEN.  
KW Postsynaptic neurotoxin; Neurotoxin; Toxin;  
KW Acetylcholine receptor inhibitor; Amidation.  
FT DISULFID 2 8  
FT DISULFID 3 16  
FT MOD\_RES 16 16 AMIDATION  
SQ SEQUENCE 16 AA; 1731 MW; 1E310FEB8FDC7001 CRC64;

Query Match 37.8%; Score 45; DB 1; Length 16;

Best Local Similarity 46.7%; Pred. No. 1.8;  
Matches 7; Conservative 2; Mismatches 6; Indels 0; Gaps 0;  
QY 1 CCSPNVPCHLEHSLC 15  
||||| :|| :||  
DB 2 CCSPPCFATNSDYC 16

## RESULT 13

ID PMP1\_CHLTP STANDARD; PRT; 878 AA.  
AC O84882;  
DT 16-OCT-2001 (Rel. 40, Created)  
DT 16-OCT-2001 (Rel. 40, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Probable outer membrane protein pmp1 precursor (Polymorphic membrane  
DE protein 1).  
DE PMP1 OR CT874.  
GN Chlamydia trachomatis.  
OC Bacteria; Chlamydiales; Chlamydiaceae; Chlamydia.  
OX NCBI\_TaxID=813;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=D/JW-3/Cx;  
RX MEDLINE=99000809; PubMed=9784136;  
RA Stephens R.S., Kallan S., Lammel C.J., Fan J., Marathe R., Aravind L.,  
RA Mitchell W.P., Olinger L., Tatusov R.L., Zhao Q., Koonin E.V.,  
RA Davis R.W.;  
RT "Genome sequence of an obligate intracellular pathogen of humans:  
RT Chlamydia trachomatis.";  
RL Science 282:754-759(1998).  
CC -!- SUBCELLULAR LOCATION: CELL WALL SURFACE (ELEMENTARY BODIES)  
CC (POTENTIAL).  
CC -!- SIMILARITY: BELONGS TO THE PMP OUTER MEMBRANE PROTEIN FAMILY.  
CC  
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DR EMBL; AE001361; AAC68472.1; -.  
DR InterPro; IPR003368; Chlamydia\_PMP.  
DR InterPro; IPR003357; OMP.  
DR Pfam; PF02385; OMP; 1.  
DR Pfam; PF02415; DUF145; 1.  
KW Outer membrane; Signal; Multigene family; Complete proteome.  
FT SIGNAL 1 24 POTENTIAL.  
FT CHAIN 25 878 PROBABLE OUTER MEMBRANE PROTEIN PMP1.  
SQ SEQUENCE 878 AA; 95592 MW; DF1F1A31707EE48B CRC64;

Query Match 37.8%; Score 45; DB 1; Length 878;  
Best Local Similarity 40.0%; Pred. No. 56;  
Matches 10; Conservative 1; Mismatches 8; Indels 6; Gaps 1;

QY 1 CCSPNVPCH-----LEHSLCTNGG 19  
||||| :|| :||  
DB 207 CCNLCISGNVNLFFTGNSATNGG 231

## RESULT 14

ID FBN2\_MOUSE STANDARD; PRT; 2907 AA.  
AC Q61555; Q63957;  
DT 15-DEC-1998 (Rel. 37, Created)  
DT 15-DEC-1998 (Rel. 37, Last sequence update)  
DT 15-JUN-2002 (Rel. 41, Last annotation update)  
DE Fibrillin 2 precursor.  
GN FBN2 OR FBN-2.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;





FT	DISULFID	952	964	BY SIMILARITY.
FT	DISULFID	952	964	BY SIMILARITY.
FT	DISULFID	959	973	BY SIMILARITY.
FT	DISULFID	975	988	BY SIMILARITY.
FT	DISULFID	1070	1082	BY SIMILARITY.
FT	DISULFID	1077	1091	BY SIMILARITY.
FT	DISULFID	1093	1106	BY SIMILARITY.
FT	DISULFID	1112	1124	BY SIMILARITY.
FT	DISULFID	1119	1133	BY SIMILARITY.
FT	DISULFID	1135	1149	BY SIMILARITY.
FT	DISULFID	1155	1167	BY SIMILARITY.
FT	DISULFID	1162	1176	BY SIMILARITY.
FT	DISULFID	1178	1191	BY SIMILARITY.
FT	DISULFID	1197	1209	BY SIMILARITY.
FT	DISULFID	1220	1218	BY SIMILARITY.
FT	DISULFID	1224	1233	BY SIMILARITY.
FT	DISULFID	1239	1250	BY SIMILARITY.
FT	DISULFID	1246	1259	BY SIMILARITY.
FT	DISULFID	1261	1274	BY SIMILARITY.
FT	DISULFID	1280	1292	BY SIMILARITY.
FT	DISULFID	1287	1301	BY SIMILARITY.
FT	DISULFID	1303	1316	BY SIMILARITY.
FT	DISULFID	1322	1334	BY SIMILARITY.
FT	DISULFID	1329	1343	BY SIMILARITY.
FT	DISULFID	1345	1358	BY SIMILARITY.
FT	DISULFID	1364	1377	BY SIMILARITY.
FT	DISULFID	1371	1386	BY SIMILARITY.
FT	DISULFID	1388	1399	BY SIMILARITY.
FT	DISULFID	1405	1418	BY SIMILARITY.
FT	DISULFID	1412	1427	BY SIMILARITY.
FT	DISULFID	1429	1440	BY SIMILARITY.
FT	DISULFID	1446	1458	BY SIMILARITY.
FT	DISULFID	1453	1467	BY SIMILARITY.
FT	DISULFID	1469	1482	BY SIMILARITY.
FT	DISULFID	1488	1499	BY SIMILARITY.
FT	DISULFID	1494	1508	BY SIMILARITY.
FT	DISULFID	1510	1523	BY SIMILARITY.
FT	DISULFID	1529	1540	BY SIMILARITY.
FT	DISULFID	1535	1549	BY SIMILARITY.
FT	DISULFID	1551	1564	BY SIMILARITY.
FT	DISULFID	1647	1659	BY SIMILARITY.
FT	DISULFID	1654	1668	BY SIMILARITY.
FT	DISULFID	1670	1683	BY SIMILARITY.
FT	DISULFID	1689	1701	BY SIMILARITY.
FT	DISULFID	1696	1710	BY SIMILARITY.
FT	DISULFID	1712	1725	BY SIMILARITY.

Query Match 37.8%; Score 45; DB 1; Length 2907;

Best Local Similarity 50.0%; Pred. No. 1.6e+02;

Matches 9; Conservative 0; Mismatches 5; Indels 4; Gaps 1;

QY	2	CSNPVCHLSHSLCTNGG	19
QY	2	CSNPVCHLSHSLCTNGG	19
Db	175	CGQPVG---ENGCGGG	188

RESULT 15

FBN2 HUMAN STANDARD; PRT; 2911 AA.

ID FBN2 HUMAN

AC P35556;

DT 01-JUN-1994 (Rel. 29, Created)

DT 01-FEB-1996 (Rel. 33, Last sequence update)

DT 15-JUN-2002 (Rel. 41, Last annotation update)

DE Fibrillin 2 precursor.

GN FBN2.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI\_TaxID=9606;

RN [1]

RN SEQUENCE FROM N.A.

RX MEDLINE=94165150; PubMed=8120105;

RX Zhang H., Apfelroth S.D., Hu W., Davis E.C., Sanguineti C., Bonadio J., Mecham R.P., Ramirez F.

"Structure and expression of fibrillin-2, a novel microfibrillar component preferentially located in elastic matrices.";

J. Cell Biol. 124:855-863(1994).

[2]

SEQUENCE OF 752-1505 FROM N.A.

MEDLINE=91304567; PubMed=1852206;

Lee B., Godfrey M., Vitale E., Hori H., Mattei M.-G., Sarfarazi M., Tsipouras P., Ramirez F., Hollister D.;

"Linkage of Marfan syndrome and a phenotypically related disorder to two different fibrillin genes.";

Nature 352:330-334(1991).

[3]

VARIANTS CCA TYR-1252 AND SER-1433, AND VARIANT ILE-964.

MEDLINE=96083599; PubMed=7493032;

Putnam E.A., Zhang H., Ramirez F., Milewicz D.M.;

"Fibrillin-2 (FBN2) mutations result in the Marfan-like disorder, congenital contractual arachnodactyly.";

Nat. Genet. 11:456-458(1995).

[4]

VARIANTS CCA HIS-1114.

MEDLINE=98407789; PubMed=9737771;

Babcock D., Gasner C., Francke U., Maslen C.;

"A single mutation that results in an asp-to-his substitution and partial exon skipping in a family with congenital contractual arachnodactyly.";

Hum. Genet. 103:22-28(1998).

[5]

VARIANTS CCA PHE-1141 AND TRP-1252.

MEDLINE=20259236; PubMed=10797416;

Belleh S., Zhou G., Wang M., Der Kaloustian V.M., Pagon R.A., Godfrey M.;

"Two novel fibrillin-2 mutations in congenital contractual arachnodactyly.";

Am. J. Med. Genet. 92:7-12(2000).

-|- FUNCTION: STRUCTURAL COMPONENT OF CONNECTIVE TISSUE MICROFIBRILS THAT BINDS CALCIUM. FIBRILLIN-2-CONTAINING MICROFIBRILS REGULATE THE EARLY PROCESS OF ELASTIC FIBER ASSEMBLY.

-|- DISEASE: DEFECTS IN FBN2 ARE THE CAUSE OF CONGENITAL CONTRACTURAL ARACHNOACTYLY (CCA) (ALSO KNOWN AS BEALS SYNDROME). CCA IS PHENOTYPICALLY SIMILAR TO MARFAN SYNDROME, BUT DOES NOT EFFECT THE AORTA AND THE EYES.

-|- SIMILARITY: CONTAINS 47 EGF-LIKE DOMAINS.

-|- SIMILARITY: CONTAINS 7 TGF-BETA BINDING PROTEIN DOMAINS.

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EMBL; U03272; AAA18950.1; -

EMBL; X62009; -; NOT\_ANNOTATED\_CDS.

PIR; S17063; S17063.

PIR; S31101; S31101.

HSSP; P35555; 1EMN.

Genew; HGNC:3604; FBN2.

MM; 121050; -

InterPro; IPR000152; Asx\_hydroxyl.

InterPro; IPR000561; EGF-like.

InterPro; IPR001881; EGF\_Ca.

InterPro; IPR001438; EGF-II.

InterPro; IPR002212; Fibril-assoc.

Pfam; PF00008; EGF; 45.

Pfam; PF0068

KW Extracellular matrix; Calcium-binding; Glycoprotein; EGF-like domain;  
 KW Repeat; Signal; Multigene family; Disease mutation; Polymorphism.

FT	1	28	POTENTIAL.	FT	DISULFID	497	509	BY SIMILARITY.
FT	CHAIN	29	FTBRULLIN 2.	FT	DISULFID	504	518	BY SIMILARITY.
FT	DOMAIN	111	EGF-LIKE 1.	FT	DISULFID	520	532	BY SIMILARITY.
FT	DOMAIN	145	EGF-LIKE 2.	FT	DISULFID	538	548	BY SIMILARITY.
FT	DOMAIN	176	EGF-LIKE 3.	FT	DISULFID	543	557	BY SIMILARITY.
FT	DOMAIN	275	EGF-LIKE 4.	FT	DISULFID	559	572	BY SIMILARITY.
FT	DOMAIN	317	EGF-LIKE 5.	FT	DISULFID	578	590	BY SIMILARITY.
FT	REPEAT	359	EGF-LIKE 6.	FT	DISULFID	585	599	BY SIMILARITY.
FT	DOMAIN	493	EGF-LIKE 7.	FT	DISULFID	601	614	BY SIMILARITY.
FT	DOMAIN	534	EGF-LIKE 8.	FT	DISULFID	620	631	BY SIMILARITY.
FT	DOMAIN	574	EGF-LIKE 9.	FT	DISULFID	626	640	BY SIMILARITY.
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FT	DOMAIN	657	EGF-LIKE 11.	FT	DISULFID	661	672	BY SIMILARITY.
FT	REPEAT	698	EGF-LIKE 12.	FT	DISULFID	667	681	BY SIMILARITY.
FT	DOMAIN	767	EGF-LIKE 13.	FT	DISULFID	683	696	BY SIMILARITY.
FT	DOMAIN	809	EGF-LIKE 14.	FT	DISULFID	771	783	BY SIMILARITY.
FT	DOMAIN	851	EGF-LIKE 15.	FT	DISULFID	778	792	BY SIMILARITY.
FT	DOMAIN	890	EGF-LIKE 16.	FT	DISULFID	794	807	BY SIMILARITY.
FT	DOMAIN	934	EGF-LIKE 17.	FT	DISULFID	813	825	BY SIMILARITY.
FT	REPEAT	996	EGF-LIKE 18.	FT	DISULFID	820	834	BY SIMILARITY.
FT	DOMAIN	1072	EGF-LIKE 19.	FT	DISULFID	836	849	BY SIMILARITY.
FT	DOMAIN	1114	EGF-LIKE 20.	FT	DISULFID	855	865	BY SIMILARITY.
FT	DOMAIN	1157	EGF-LIKE 21.	FT	DISULFID	860	874	BY SIMILARITY.
FT	DOMAIN	1199	EGF-LIKE 22.	FT	DISULFID	876	889	BY SIMILARITY.
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FT	DOMAIN	1282	EGF-LIKE 24.	FT	DISULFID	958	970	BY SIMILARITY.
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FT	DOMAIN	1366	EGF-LIKE 26.	FT	DISULFID	981	994	BY SIMILARITY.
FT	DOMAIN	1407	EGF-LIKE 27.	FT	DISULFID	1076	1088	BY SIMILARITY.
FT	DOMAIN	1448	EGF-LIKE 28.	FT	DISULFID	1083	1097	BY SIMILARITY.
FT	DOMAIN	1490	EGF-LIKE 29.	FT	DISULFID	1099	1112	BY SIMILARITY.
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FT	DOMAIN	1649	EGF-LIKE 32.	FT	DISULFID	1141	1155	BY SIMILARITY.
FT	DOMAIN	1691	EGF-LIKE 33.	FT	DISULFID	1161	1173	BY SIMILARITY.
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FT	DOMAIN	1891	EGF-LIKE 37.	FT	DISULFID	1210	1224	BY SIMILARITY.
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FT	DOMAIN	2170	EGF-LIKE 43.					
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FT	DOMAIN	2251	EGF-LIKE 45.					
FT	DOMAIN	2292	EGF-LIKE 46.					
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FT	REPEAT	2379	EGF-LIKE 49.					
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Query Match 37.8%; Score 45; DB 1; Length 2911;  
 Best Local Similarity 50.0%; Pred. NO. 1.6e+02;  
 Matches 9; Conservative 0; Mismatches 5; Indels 4; Gaps 1;

Oy 2 CSNPVCHLEHNSNLCNNGG 19  
 Db 175 CGQPCV-----ENGCONGG 188

Search completed: March 17, 2003, 07:24:21  
 Job time : 6.06107 secs